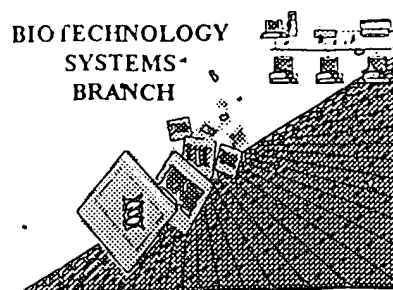


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/892613

Source: OIPÉ

Date Processed by STIC: 11/26/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

SEQUENCE LISTING

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(1) General Information:

Applicant name

Title of invention

Number of sequences

are required.

ERRORED SEQUENCES FOLLOW:

Mailing Address is required

① Gross Format Errors
See Attached Template
See pages 2, 3, and 4
Does Not Comply
Corrected Diskette Needed

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligonucleotide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

④ An integer response is mandatory in the length field

FR-patched RFB4

VH+

Full length cDNA sequence (SEQ ID no. 1):

GAAGTGCAGCTGCTGGAGTCTGGGGGAGGCTTAGTGCAGCCTGGAGGGTCCCTGAGGCTCTCCTGTGCAGCCTCTGGATT
CTCCTTCAGTATCTATGACATGTCTTGGGTTCCGAGGACCGGGAAAGGGGCTGGAGTGGGTTCGCATACATTAGTAGTG
GTGGTGGTACCACCTACTATCCAGACACTGTGAAGGGCCGATTACCATCTCCAGAGACAATGCCAAGAACTCCCTGTAC
CTGCAAATGAACAGTCTGAGGGTGGAGGACACAGCCTTATATTACTGTGCAAGACATAGTGGCTACGGTAGTAGCTACGG
GGTTTGTGTTGCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTTCA

Full length amino acid sequence (SEQ ID no. 2):

EVQLLESGGGLVQPGSLRLSCAASGFSFSIYDMSWVRQAPGKLEWVAYISSGGGTTYYPDTVKGRTISRDNKNSLY
LQMNLSLRVEDTALYYCARHSGYGSSYGVLFAYWQGQTLVTVSS

N-terminal sense strand template DNA sequence (SEQ ID no. 3):

CCTGGAGGGTCCCTGAGGCTCTCCTGTGCAGCCTCTGGATTCTCCTTCAGTATCTATGACATGTCTTGGGTTCCGAGGC
ACCGGGAAAGGGGCTGGAGTGGGTTCGCATAC

5' Primer for N-template (SEQ ID no. 4)

GAAGTGCAGCTGCTGGAGTCTGGGGGAGGCTTAGTGCAGCCTGGAGGGTCCCTGAGG

3' Primer for N-template (SEQ ID no. 5)

GTAGGTGGTACCACCACCACTACTAATGTATGCGACCACTCCAGCCC

OK for Sequence characteristics

OK for Sequence characteristics

⑤ See Attached template for required fields.

⑥ Refer to Federal Register Vol 55 No 84 Tuesday May 1, 1990
CFR in 37 CFR Part 1 § 1.821 - § 1.825
for ~~other~~ specific guidelines and requirements.

Start of Format Required for each sequence

invalid formats

Gene Sequence Template

RECEIVED
 AUG 28 2002
 TECH CENTER 1600/2900
 Mandating
 Introductory
 Information
 From Applicant

1) GENERAL INFORMATION:

1.1 APPLICANT:

1.2 TITLE OF INVENTION:

1.3 NUMBER OF SEQUENCES:

1.4 CORRESPONDENCE ADDRESS:

1.5 ADDRESSEE:

1.6 STREET:

1.7 CITY:

1.8 STATE:

1.9 COUNTRY:

1.10 ZIP:

1.11 COMPUTER READABLE FORM:

1.12 MEDIUM TYPE:

1.13 COMPUTER:

1.14 OPERATING SYSTEM:

1.15 SOFTWARE:

1.16 CURRENT APPLICATION DATA:

1.17 APPLICATION NUMBER:

1.18 FILING DATE:

1.19 CLASSIFICATION:

1.20 PRIOR APPLICATION DATA:

1.21 APPLICATION NUMBER:

1.22 FILING DATE:

1.23 ATTORNEY/AGENT INFORMATION:

1.24 NAME:

1.25 REGISTRATION NUMBER:

1.26 REFERENCE/DOCKET NUMBER:

1.27 TELECOMMUNICATION INFORMATION:

1.28 TELEPHONE:

1.29 TELEFAX:

1.30 TELEX:

2) INFORMATION FOR SEQ ID NO. X:

2.1 SEQUENCE CHARACTERISTICS:

2.2 LENGTH:

2.3 TYPE:

2.4 STRANDEDNESS:

2.5 TOPOLOGY:

2.6 MOLECULE TYPE:

2.7 ISOTOPICTICAL:

2.8 ANTI-SENSE:

2.9 FRAGMENT TYPE:

2.10 ORIGINAL SOURCE:

2.11 ORGANISM:

2.12 STRAIN:

2.13 INDIVIDUAL ISOLATE:

2.14 DEVELOPMENTAL STAGE:

2.15 HAPLOTYPE:

2.16 TISSUE TYPE:

2.17 CELL TYPE:

2.18 CELL LINE:

2.19 ORGANELLE:

2.20 IMMEDIATE SOURCE:

2.21 LIBRARY:

2.22 CLONE:

2.23 POSITION IN GENOME:

2.24 CHROMOSOME/SEGMENT:

2.25 MAP POSITION:

2.26 UNITS:

2.27 FEATURE:

2.28 NAME/KEY:

2.29 LOCATION:

2.30 IDENTIFICATION METHOD:

2.31 OTHER INFORMATION:

3) PUBLICATION INFORMATION:

3.1 AUTHORS:

3.2 TITLE:

3.3 JOURNAL:

3.4 VOLUME:

3.5 ISSUE:

3.6 PAGES:

3.7 DATE:

3.8 DOCUMENT NUMBER:

3.9 FILING DATE:

3.10 PUBLICATION DATE:

4) RELEVANT RESIDUES:

5) SEQUENCE DESCRIPTION: SEQ ID NO. X:

These fields
 are mandatory

These fields
 are mandatory
 for each gene sequence

Optional fields for
 possibly applicable
 information

Please follow this guideline and rules in 37 CFR § 1.821-1.2.

1. applicant context fields are required
2. sequence id descriptions are required
3. Publication information is ~~to be provided~~ optional
 If applicable, you may choose to provide it.

RAW SEQUENCE LISTING PATENT APPLICATION US/09/892,613

DATE: 11/26/2001
TIME: 02:32:10

INPUT SET: S36677.raw

--> 40 C-terminal sense strand template DNA sequence (SEQ ID no. 6):
41 TTCACCATCTCCAGAGACAATGCCAAGAACTCCCTGTACCTGCAAATGAACAGTCTGAGGGTGGAGGACACAGCCTTATA
42 TTACTGTGCAAGACATAGTGGCTACGGTAGTAGCTACGGGGTTTTGTTTGCT
43
--> 44 5' Primer for C-template (SEQ ID no. 7)
45 GGTGGTACCACCTACTATCCAGACACTGTGAAGGGCCGATTACCATCTCCAGAGACAAT
46
--> 47 3' Primer for C-template (SEQ ID no. 8)
48 TGAAGAGACAGTGACCAGAGTCCCTTGGCCCCAGTAAGCAAACAAAACCCCGTAGCT
49
50 Joining site: KpnI
51
52 VK: *type nucleic acid*
53 *ii molecule type c DNA etc.*
54 Full length cDNA sequence (SEQ ID no. 9) *see template*
55 GATATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTGGGAGACAGAGTCACCATTAGTTGCAGGGCAAGTCA
56 GGACATTAGCAATTATTTAAACTGGTATCAGCAGAAACCAGGTAAGGCTCCGAAACTCCTGATCTACTACACTAGTATAT
57 TACACTCAGGAGTCCCATCAAGGTTCACTGGCAGTGGGTCTGGAACAGAATTTACTCTCACCATTAGCTCCCTGCAGCCA
58 GAAGATTTTGCCACTTACTTTTGCCAAACAGGGTAATACGCTTCCGTGGACGTTCCGTGGAGGCACCAAGGTGGAAATCAA
59 A
60
61 Full length amino acid sequence (SEQ ID no. 10) *A length integer*
62 DIQMTQSPSSLSASVGRVTISCRASQDISNYLNWYQQKPKAPKLLIYYTSLHSGVPSRFSGSGSGTEFTLTISLQ
63 EDFATYFCQQGNTLPWTFGGGTVKVEIK *C not relevant*
64
65 N-terminal sense strand template DNA sequence (SEQ ID no. 11) *D shape not relevant*
66 CTGTCTGCCTCTGTGGGAGACAGAGTCACCATTAGTTGCAGGGCAAGTCAGGACATTAGCAATTATTTAAACTGGTATCA
67 GCAGAAACCAGGTAAGGCTCCGAAACTC *ii blank*
68
69 5' Primer for N template (SEQ ID no. 12) *A Description proteins*
70 GATATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTGGGAGAC
71
72 3' Primer for N-template (SEQ ID no. 13)
73 ATATACTAGTGTAGTAGATCAGGAGTTTCGGAGCCTTACC
74
75 C-terminal sense strand template DNA sequence (SEQ ID no. 14) *etc. are mandatory*
76 CCATCAAGGTTCACTGGCAGTGGGTCTGGAACAGAATTTACTCTCACCATTAGCTCCCTGCAGCCAGAAGATTTGCCAC
77 TTACTTTTGCCAAACAGGGTAATACGCTTCCGTGGACGTTCC
78
79 5' Primer for C-template (SEQ ID no. 15)
80 CTACACTAGTATATTACACTCAGGAGTCCCATCAAGGTTCACTGGCAGT
81
82 3' Primer for C-template (SEQ ID no. 16)
83 TTTGATTTCCACCTTGGTGCTCCACCGAAGCTCCAGGAAGCGTATT
84
85 Joining site: SpeI A(CTAG(T
86
87
88 FR-Patched chimeric 1F5
89
90 VH:
91
92 Full length cDNA sequence (SEQ ID no. 17):

Each sequence must be identified according to the rules, template and enclosed example corrections

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/892,613DATE: 11/26/2001
TIME: 02:32:10

INPUT SET: S36677.raw

93 CAGGTGCAACTGGTGGCTTCCGGGGCTGAGGTAAATAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGGCTA
94 CACATTTACCAGTTACAATATGCACTGGGTACGGCAGCCTCCTGGAAGGGGCTGGAATGGATTGGAGCTATTTATCCAG
95 GAAATGGTGATACTAGTTACAATCAGAAATCAAGGGCAAGGCCACATTGACTGCAGACAAATCCTCCAGCACAGCCTAC
96 ATGCAGCTCAGCAGTCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCGCACTACGGTAGTAACCTACGTAGA
97 CTACTTTGACTACTGGGGCCAAGGCACCACTGTTACAGTCTCCTCTGATCA
98
--> 99 Full-length amino acid sequence (SEQ ID no. 18):
100 QVQLVASGAENVKPGASVKVSKASGYTFTSYNMHWVRQPPGRGLEWIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAY
101 MQLSSLTSEDSAVYYCARSHYGSNYVDYFDYWGQGTITVTVSSD
102
103 *2. sequence characteristics: molecule type*
--> 104 N-terminal sense strand template DNA sequence (SEQ ID no. 19):
105 AATAAGCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTACG
106 GCAGCCTCCTGGAAGGGGCTGGAATGGATTGGA
107
--> 108 5' Primer for N-template (SEQ ID no. 20)
109 CAGGTGCAACTGGTGGCTTCCGGGGCTGAGGTAAATAAGCCTGGGGCCTCAGTGAAG
110
--> 111 3' Primer for N-template (SEQ ID no. 21)
112 TGTAAGTAGTATCACCATTTCCTGGATAAATAGCTCCAATCCATTCCAGGCCCT
113
--> 114 C-terminal sense strand template DNA sequence (SEQ ID no. 22):
115 TTGACTGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGTCTGACATCTGAGGACTCTGCGGTCTATTACTG
116 TGCAAGATCGCACTACGGTAGTAACCTACGTAGACTACTTTGACTAC
117
--> 118 5' Primer for C-template (SEQ ID no. 23)
119 TGATACTAGTTACAATCAGAAATCAAGGGCAAGGCCACATTGACTGCAGACAAATCCTCC
120
--> 121 3' Primer for C-template (SEQ ID no. 24)
122 TGATCAGAGGAGACTGTAACAGTGGTGCCTTGGCCCCAGTAGTCAAAGTAGTCTACGTA
123
124 Joining site: SpeI
125
126 VK:
127
128 *Full-length cDNA sequence (SEQ ID no. 25):*
129 GATATTCAACTCACACAGTCTCCATCAAGTCTTTCTGCATCTGTGGGGGACAGAGTCACAATTACTTGCAGGGCCAGCTC
130 AAGTTTAAAGTTTCATGCACTGGTACCAGCAGAAGCCAGGATCCTCCCCCAAACCTGGATTATGCCACATCCAACCTGG
131 CTTCCGGAGTCCCTAGTCGCTTCAGTGGCAGTGGGTCTGGGACCGAGTTCACTCTACAATCAGCAGTTTGCAGCCTGAA
132 GATTCGCCACTTATTTCTGCCATCAGTGGAGTAGTAACCCGCTCACGTTCCGGTGCTGGGACCAAGCTGACCGTTCTACG
133 G
134
--> 135 Full-length amino acid sequence (SEQ ID no. 26):
136 DIQLTQSPSSLSASVGDRTITCRASSLSFMHWYQQKPGSSPKPWIYATSNLASGVPSRFSGSGSGTEFTLTISSLQPE
137 DFATYFCHQWSSNPLTFGAGTKLTVLR
138
--> 139 N-terminal sense strand template DNA sequence (SEQ ID no. 27):
140 TCAAGTCTTTCTGCATCTGTGGGGGACAGAGTCACAATTACTTGCAGGGCCAGCTCAAGTTTAAGTTTCATGCACTGGTA
141 CCAGCAGAAGCCAGGATCCTCCCCCAAACCTGGATTATGCCACATCC
142
--> 143 5' Primer for N-template (SEQ ID no. 28):
144 GATATTCAACTCACACAGTCTCCATCAAGTCTTTCTGCATCTGTG
145

*B. Type
C. 3 strandedness
D. Topology*

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/892,613DATE: 11/26/2001
TIME: 02:32:11

INPUT SET: S36677.raw

--> 146 3' Primer for N-template (SEQ ID no. 29):
147 GGACTCCGGAAGCCAGGTTGGATGTGGCATAAATCCAGGG
148
--> 149 C-terminal sense strand template DNA sequence (SEQ ID no. 30):
150 TTCAGTGGCAGTGGGTCTGGGACCGAGTTCACCTCTACAATCAGCAGTTTGCAGCCTGAAGATTTGCGCCACTTATTTCTG
151 CCATCAGTGGAGTAGTAACCCGCTCACGTTCCGGTGCTGGG
152
--> 153 5' Primer for C-template (SEQ ID no. 31):
154 GGCTTCCGGAGTCCCTAGTCGCTTCAGTGGCAGTGGGTCTGGG
155
--> 156 3' Primer for C-template (SEQ ID no. 32):
157 CCGTAGAACGGTCAGCTTGGTCCCAGCACCGAACGTGAGCGG
158
159 Joining site: BspEI
160
161

1. Lines 5-12 are the beginning of an extended format required for sequence listings.
2. Refer to the rules in 37 CFR Part 1 Rules of Practice in Patent Cases according to § 1.821 - § 1.825
(Set forth in The Federal Register Vol 55, No 84
Tuesday, May 1, 1990 — Rules and Regulations)
3. Use the Template attached and the CFR rules as a guide
4. Call Mark Spencer at the Help Desk
for additional assistance 203 308 4212